

REMARKS

Formal Matters

The present application has been amended to insert the Sequence Listing, and to amend the specification to contain the requisite reference to the sequences listed in the Sequence Listing. No new matter is added.

Certification Regarding Sequence Listing

I hereby certify that the enclosed Sequence Listing is being submitted under 37 CFR §§ 1.821(c) and (e) in paper and computer readable form (Compact Disk labeled 'CRF').

As required by 37 CFR 1.821(f), I hereby state that the content of the paper and computer readable copy of the Sequence Listing, submitted in accordance with 37 C.F.R. §1.821(c) and (e) are the same. The Computer Readable Format (CRF), being submitted under 37 CFR §§ 1.52(e) and 1.824, is formatted on IBM-PC, the operating system compatibility is MS-Windows and the file listing is:

Seqlist.txt 20.6 KB created December 10, 2002.

I hereby certify that the enclosed submission includes no new matter. The Sequence Listing was prepared with the software FASTSEQ, and conforms to the Patent Office guidelines. Applicant respectfully submits that the subject application is in adherence to 37 CFR §§ 1.821-1.825.

Respectfully submitted,

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“Version with Markings to Show Changes”

In the specification:

Please replace the paragraph on page 44, starting on line 12 with the following paragraph:

A. Three cDNA clones which encode three different human homologs for C6ST/KSST have been obtained. The predicted GST proteins are type 2 membrane proteins 411, 484, and 386 amino acids in length, respectively. Each has a relatively short transmembrane domain and a short amino-terminal cytoplasmic tail. Table 2 demonstrates the high homologies among the 3 human proteins and the chick CS6T/KSST. Overall homologies at the amino acid level ranged from 28% to 40% identity. Strikingly, there are three regions of 16 to 29 amino acids in which identity among the three GSTs ranged from 50-59% and similarity ranged from 65-94%. All four of the sulfotransferases are type II transmembrane proteins with short cytoplasmic tails. There are three regions (region A, B and C) in which identities among the human GSTs range from 50-59% and similarities range from 65 to 94%. The amino acid sequence for the regions are:

A: (T/S)XRSGSSF(V/F)G(Q/E)LFXQX(P/L)(D/E)VF(F/Y)L(F/Y/M)EP(L/V/A)(W/Y)HV
(SEQ ID NO: 33)

B: L(N/D)L(K/H)(V/I)(I/V)XLVRDPR(A/G)(V/I)(LAF) (SEQ ID NO: 34)

C: PXXL(Q/K)XXY(L/M)(L/V)VRYEDL(A/V)XXP (SEQ ID NO: 35)

Please replace the paragraph on page 57, starting on line 2 with the following paragraph:

For the RT-PCR analysis of the F2 mice, total RNA was purified from peripheral lymph nodes and mesenteric lymph nodes of HEC-GlcNAc6ST +/+ and -/- mouse by lysis and extraction with RNAZol (Tel-Test Inc, Friendwood, Texas). cDNA was synthesized from the total RNA using random hexamers for priming and AMV reverse transcriptase. PCR reactions were carried with the cDNAs and the following primers pairs:

KSGal6ST:

5' primer: 5'-AGTCATGTGGCCATCAAGACTGTGCGGGTG
3' Primer: 5'-GGGAGATAAGGCAACAGTTAAAGACGGCCC
(SEQ ID NOS: 10 & 11)

HEC-GlcNAc6ST:

5' primer: 5'-CATGGGTCAGCATGCCTTCCATACTAACGCCA

3' primer: 5'-CTCTGCTTGGGCTGAGGAGAAAGGGGCACTC

(SEQ ID NOS: 12 & 13)

GlcNAc6ST:

5' primer: 5'-GCCTACCGCAAGGAGGTCGTCGGACTGGTGGAC

3' primer: 5'-ACTGTTAACCGCTCATAGCCCAGCACGGCCAT

(SEQ ID NOS: 14 & 15)

HPRT:

5' primer: 5'-CCTGCTGGATTACATCAAAGCACTG

3' primer: 5'-TCCAACACTTCGTGGGTCCT

[(SEQ ID NOS: 16 & 17)] (SEQ ID NOS: 16 and 17).